

[illegible]

	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100	2101	2102	2103	2104	2105	2106	2107	2108	2109	2110	2111	2112	2113	2114	2115	2116	2117	2118	2119	2120	2121	2122	2123	2124	2125	2126	2127	2128	2129	2130	2131	2132	2133	2134	2135	2136	2137	2138	2139	2140	2141	2142	2143	2144	2145	2146	2147	2148	2149	2150	2151	2152	2153	2154	2155	2156	2157	2158	2159	2160	2161	2162	2163	2164	2165	2166	2167	2168	2169	2170	2171	2172	2173	2174	2175	2176	2177	2178	2179	2180	2181	2182	2183	2184	2185	2186	2187	2188	2189	2190	2191	2192	2193	2194	2195	2196	2197	2198	2199	2200	2201	2202	2203	2204	2205	2206	2207	2208	2209	2210	2211	2212	2213	2214	2215	2216	2217	2218	2219	2220	2221	2222	2223	2224	2225	2226	2227	2228	2229	2230	2231	2232	2233	2234	2235	2236	2237	2238	2239	2240	2241	2242	2243	2244	2245	2246	2247	2248	2249	2250	2251	2252	2253	2254	2255	2256	2257	2258	2259	2260	2261	2262	2263	2264	2265	2266	2267	2268	2269	2270	2271	2272	2273	2274	2275	2276	2277	2278	2279	2280	2281	2282	2283	2284	2285	2286	2287	2288	2289	2290	2291	2292	2293	2294	2295	2296	2297	2298	2299	2300	2301	2302	2303	2304	2305	2306	2307	2308	2309	2310	2311	2312	2313	2314	2315	2316	2317	2318	2319	2320	2321	2322	2323	2324	2325	2326	2327	2328	2329	2330	2331	2332	2333	2334	2335	2336	2337	2338	2339	2340	2341	2342	2343	2344	2345	2346	2347	2348	2349	2350	2351	2352	2353	2354	2355	2356	2357	2358	2359	2360	2361	2362	2363	2364	2365	2366	2367	2368	2369	2370	2371	2372	2373	2374	2375	2376	2377	2378	2379	2380	2381	2382	2383	2384	2385	2386	2387	2388	2389	2390	2391	2392	2393	2394	2395	2396	2397	2398	2399	2400	2401	2402	2403	2404	2405	2406	2407	2408	2409	2410	2411	2412	2413	2414	2415	2416	2417	2418	2419	2420	2421	2422	2423	2424	2425	2426	2427	2428	2429	2430	2431	2432	2433	2434	2435	2436	2437	2438	2439	2440	2441	2442	2
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<subunit 1 of 1, 379 aa, 1 stop

MKEYVLLLLFLALCSAKPFFSPSHIALKNMMLKDMEDTDDDDDDDDDDDDDDDEDNSLFPTREPR
SHFFPFDLFP MCPFGCQCYSRVVHCSDLGLTSVPTNIPFDTRMLDLQNNKIKEIKENDFKGL
TSLYGLILNNNKLTKIHPKAFLTTKKLRRRLYLSHNQLSEIPLNLPKSLAELRIHENKVKKIQ
KDTFKGMNALHVLEMSANPLDNNGIEPGAFEGVTVFHIRIAEAKLTSVPKGLPPTLLELHLD
YNKISTVELEDFKRYKELQRLGLGNNKITDIENGLANI PRVREIHLENNKLKKIPSGLP
KYLQII FLHSNSIARVGVNDFCPTVPKMKKS LYS AISLFNNPVKYWEMQPATFRCVLSRMSV
OLGNFGM

amino acids 1-15

amino acids 281-285

amino acids 129-135, 210-216, 214-220, 237-243, 270-276, 282-288

amino acids 154-176

[illegible]

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.5	20	55
Gender	Male	Female	Male	Female
Marital status	Married	Single	Married	Single
Education	High school	College	High school	College
Occupation	Manager	Worker	Manager	Worker
Income	\$10,000	\$20,000	\$5,000	\$30,000
Health status	Good	Poor	Good	Poor
Exercise frequency	Weekly	Monthly	Weekly	Monthly
Stress level	Low	High	Low	High
Sleep quality	Good	Poor	Good	Poor
Dietary habits	Healthy	Unhealthy	Healthy	Unhealthy
Alcohol consumption	None	Occasional	None	Occasional
Tobacco use	Non-smoker	Smoker	Non-smoker	Smoker
Family size	2	3	1	4
Home ownership	Owner	Renter	Owner	Renter
Commute time	15 min	30 min	10 min	45 min
Neighborhood safety	Safe	Unsafe	Safe	Unsafe
Access to green spaces	Yes	No	Yes	No
Proximity to public transport	Close	Far	Close	Far
Local amenities	Many	Few	Many	Few
Community involvement	Active	Passive	Active	Passive
Perceived quality of life	High	Low	High	Low

FIGURE 6

><subunit 1 of 1, 737 aa, 1 stop

><MW: 78475, pI: 5.09, NX(S/T): 11

MQPRRAQAPGAQLLPALALLLLLLGAGPRGSSLANPVPAAPLSAPGPCAAQPCRNGGVCTSR
PEPDPQHPAPAGEPGYSCTCPAGISGANQQLVADPCASNPCHHGNCSSSSSSSSSDGYLCICN
EGYEGPNCEQALPSLPATGWTESMAPRQLQPVPATQEPDKILPRSQATVTLPTWQPKTGQKV
VEMKWDQVEVIPDIACGNASSNSSAGGRLVSFEVPQNTSVKIRQDATASLILLWKVTATGFQ
QCSLIDGRSVTPLQASGGLVLLLEMLALGNNHFIGFVNDSVTKSIVALRLTLVVKVSTCVPG
ESHANDLECSGKGKCTTKPSEATFSCTCEEQYVGTFCEEYDACQRKPCQNNASCIDANEKQD
GSNFTCVCLPGYTGELCQSKIDYCIIDPCRNGATCISSLSGFTCQCPEGYFGSACEEKVDPC
ASSPCQNNGTCYVDGVHFTCNCSPGFTGPTCAQLIDFCALSPCAHGTCRSVGTSYKCLCDPG
YHGLYCEEEYNECLSAAPCLNAATCRDLVNGYECVCLAELYKGTHTCELYKDPCANVSCLNGATC
DSDGLNGTCICAPGFTGEECDIDINECDSNPCHHGGSCLDQPNGYNCHCPHGWVGANCEIHL
QWKSGHMAESLTNMPRHSlyIIIGALCVAFILMLIILIVGICRISRIEYQGSSSRPAYEEFYN
CRSIDSEFSNAIASIRHARFGKKSRPAMYDVSPiAYEDYSPDDKPLVTliKTKDL

Signal sequence.

amino acids 1-28

Transmembrane domain.

amino acids 641-660

N-glycosylation sites.

amino acids 107-111, 204-208, 208-212, 223-227, 286-290, 361-365,
375-379, 442-446, 549-553, 564-568

Glycosaminoglycan attachment site.

amino acids 320-324

Tyrosine kinase phosphorylation sites.

amino acids 490-498, 674-682

N-myristoylation sites.

amino acids 30-36, 56-62, 57-63, 85-91, 106-112, 203-209,
373-379, 449-455, 480-486, 562-568, 565-571

Amidation site.

amino acids 702-706

Aspartic acid and asparagine hydroxylation site.

amino acids 520-532, 596-608

EGF-like domain cysteine pattern signatures.

amino acids 80-92, 121-133, 336-348, 378-390, 416-428, 454-466,
491-503, 529-541, 567-579, 605-617

1. 2000-2001 2. 2002-2003 3. 2004-2005 4. 2006-2007 5. 2008-2009 6. 2010-2011 7. 2012-2013 8. 2014-2015 9. 2016-2017 10. 2018-2019 11. 2020-2021 12. 2022-2023 13. 2024-2025 14. 2026-2027 15. 2028-2029 16. 2030-2031 17. 2032-2033 18. 2034-2035 19. 2036-2037 20. 2038-2039 21. 2040-2041 22. 2042-2043 23. 2044-2045 24. 2046-2047 25. 2048-2049 26. 2050-2051 27. 2052-2053 28. 2054-2055 29. 2056-2057 30. 2058-2059 31. 2060-2061 32. 2062-2063 33. 2064-2065 34. 2066-2067 35. 2068-2069 36. 2070-2071 37. 2072-2073 38. 2074-2075 39. 2076-2077 40. 2078-2079 41. 2080-2081 42. 2082-2083 43. 2084-2085 44. 2086-2087 45. 2088-2089 46. 2090-2091 47. 2092-2093 48. 2094-2095 49. 2096-2097 50. 2098-2099 51. 2100-2101 52. 2102-2103 53. 2104-2105 54. 2106-2107 55. 2108-2109 56. 2110-2111 57. 2112-2113 58. 2114-2115 59. 2116-2117 60. 2118-2119 61. 2120-2121 62. 2122-2123 63. 2124-2125 64. 2126-2127 65. 2128-2129 66. 2130-2131 67. 2132-2133 68. 2134-2135 69. 2136-2137 70. 2138-2139 71. 2140-2141 72. 2142-2143 73. 2144-2145 74. 2146-2147 75. 2148-2149 76. 2150-2151 77. 2152-2153 78. 2154-2155 79. 2156-2157 80. 2158-2159 81. 2160-2161 82. 2162-2163 83. 2164-2165 84. 2166-2167 85. 2168-2169 86. 2170-2171 87. 2172-2173 88. 2174-2175 89. 2176-2177 90. 2178-2179 91. 2180-2181 92. 2182-2183 93. 2184-2185 94. 2186-2187 95. 2188-2189 96. 2190-2191 97. 2192-2193 98. 2194-2195 99. 2196-2197 100. 2198-2199 101. 2200-2201 102. 2202-2203 103. 2204-2205 104. 2206-2207 105. 2208-2209 106. 2210-2211 107. 2212-2213 108. 2214-2215 109. 2216-2217 110. 2218-2219 111. 2220-2221 112. 2222-2223 113. 2224-2225 114. 2226-2227 115. 2228-2229 116. 2230-2231 117. 2232-2233 118. 2234-2235 119. 2236-2237 120. 2238-2239 121. 2240-2241 122. 2242-2243 123. 2244-2245 124. 2246-2247 125. 2248-2249 126. 2250-2251 127. 2252-2253 128. 2254-2255 129. 2256-2257 130. 2258-2259 131. 2260-2261 132. 2262-2263 133. 2264-2265 134. 2266-2267 135. 2268-2269 136. 2270-2271 137. 2272-2273 138. 2274-2275 139. 2276-2277 140. 2278-2279 141. 2280-2281 142. 2282-2283 143. 2284-2285 144. 2286-2287 145. 2288-2289 146. 2290-2291 147. 2292-2293 148. 2294-2295 149. 2296-2297 150. 2298-2299 151. 2300-2301 152. 2302-2303 153. 2304-2305 154. 2306-2307 155. 2308-2309 156. 2310-2311 157. 2312-2313 158. 2314-2315 159. 2316-2317 160. 2318-2319 161. 2320-2321 162. 2322-2323 163. 2324-2325 164. 2326-2327 165. 2328-2329 166. 2330-2331 167. 2332-2333 168. 2334-2335 169. 2336-2337 170. 2338-2339 171. 2340-2341 172. 2342-2343 173. 2344-2345 174. 2346-2347 175. 2348-2349 176. 2350-2351 177. 2352-2353 178. 2354-2355 179. 2356-2357 180. 2358-2359 181. 2360-2361 182. 2362-2363 183. 2364-2365 184. 2366-2367 185. 2368-2369 186. 2370-2371 187. 2372-2373 188. 2374-2375 189. 2376-2377 190. 2378-2379 191. 2380-2381 192. 2382-2383 193. 2384-2385 194. 2386-2387 195. 2388-2389 196. 2390-2391 197. 2392-2393 198. 2394-2395 199. 2396-2397 200. 2398-2399 201. 2400-2401 202. 2402-2403 203. 2404-2405 204. 2406-2407 205. 2408-2409 206. 2410-2411 207. 2412-2413 208. 2414-2415 209. 2416-2417 210. 2418-2419 211. 2420-2421 212. 2422-2423 213. 2424-2425 214. 2426-2427 215. 2428-2429 216. 2430-2431 217. 2432-2433 218. 2434-2435 219. 2436-2437 220. 2438-2439 221.	
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1. 2000-2001 2. 2002-2003 3. 2004-2005 4. 2006-2007 5. 2008-2009 6. 2010-2011 7. 2012-2013 8. 2014-2015 9. 2016-2017 10. 2018-2019 11. 2020-2021 12. 2022-2023 13. 2024-2025 14. 2026-2027 15. 2028-2029 16. 2030-2031 17. 2032-2033 18. 2034-2035 19. 2036-2037 20. 2038-2039 21. 2040-2041 22. 2042-2043 23. 2044-2045 24. 2046-2047 25. 2048-2049 26. 2050-2051 27. 2052-2053 28. 2054-2055 29. 2056-2057 30. 2058-2059 31. 2060-2061 32. 2062-2063 33. 2064-2065 34. 2066-2067 35. 2068-2069 36. 2070-2071 37. 2072-2073 38. 2074-2075 39. 2076-2077 40. 2078-2079 41. 2080-2081 42. 2082-2083 43. 2084-2085 44. 2086-2087 45. 2088-2089 46. 2090-2091 47. 2092-2093 48. 2094-2095 49. 2096-2097 50. 2098-2099 51. 2100-2101 52. 2102-2103 53. 2104-2105 54. 2106-2107 55. 2108-2109 56. 2110-2111 57. 2112-2113 58. 2114-2115 59. 2116-2117 60. 2118-2119 61. 2120-2121 62. 2122-2123 63. 2124-2125 64. 2126-2127 65. 2128-2129 66. 2130-2131 67. 2132-2133 68. 2134-2135 69. 2136-2137 70. 2138-2139 71. 2140-2141 72. 2142-2143 73. 2144-2145 74. 2146-2147 75. 2148-2149 76. 2150-2151 77. 2152-2153 78. 2154-2155 79. 2156-2157 80. 2158-2159 81. 2160-2161 82. 2162-2163 83. 2164-2165 84. 2166-2167 85. 2168-2169 86. 2170-2171 87. 2172-2173 88. 2174-2175 89. 2176-2177 90. 2178-2179 91. 2180-2181 92. 2182-2183 93. 2184-2185 94. 2186-2187 95. 2188-2189 96. 2190-2191 97. 2192-2193 98. 2194-2195 99. 2196-2197 100. 2198-2199 101. 2200-2201 102. 2202-2203 103. 2204-2205 104. 2206-2207 105. 2208-2209 106. 2210-2211 107. 2212-2213 108. 2214-2215 109. 2216-2217 110. 2218-2219 111. 2220-2221 112. 2222-2223 113. 2224-2225 114. 2226-2227 115. 2228-2229 116. 2230-2231 117. 2232-2233 118. 2234-2235 119. 2236-2237 120. 2238-2239 121. 2240-2241 122. 2242-2243 123. 2244-2245 124. 2246-2247 125. 2248-2249 126. 2250-2251 127. 2252-2253 128. 2254-2255 129. 2256-2257 130. 2258-2259 131. 2260-2261 132. 2262-2263 133. 2264-2265 134. 2266-2267 135. 2268-2269 136. 2270-2271 137. 2272-2273 138. 2274-2275 139. 2276-2277 140. 2278-2279 141. 2280-2281 142. 2282-2283 143. 2284-2285 144. 2286-2287 145. 2288-2289 146. 2290-2291 147. 2292-2293 148. 2294-2295 149. 2296-2297 150. 2298-2299 151. 2300-2301 152. 2302-2303 153. 2304-2305 154. 2306-2307 155. 2308-2309 156. 2310-2311 157. 2312-2313 158. 2314-2315 159. 2316-2317 160. 2318-2319 161. 2320-2321 162. 2322-2323 163. 2324-2325 164. 2326-2327 165. 2328-2329 166. 2330-2331 167. 2332-2333 168. 2334-2335 169. 2336-2337 170. 2338-2339 171. 2340-2341 172. 2342-2343 173. 2344-2345 174. 2346-2347 175. 2348-2349 176. 2350-2351 177. 2352-2353 178. 2354-2355 179. 2356-2357 180. 2358-2359 181. 2360-2361 182. 2362-2363 183. 2364-2365 184. 2366-2367 185. 2368-2369 186. 2370-2371 187. 2372-2373 188. 2374-2375 189. 2376-2377 190. 2378-2379 191. 2380-2381 192. 2382-2383 193. 2384-2385 194. 2386-2387 195. 2388-2389 196. 2390-2391 197. 2392-2393 198. 2394-2395 199. 2396-2397 200. 2398-2399 201. 2400-2401 202. 2402-2403 203. 2404-2405 204. 2406-2407 205. 2408-2409 206. 2410-2411 207. 2412-2413 208. 2414-2415 209. 2416-2417 210. 2418-2419 211. 2420-2421 212. 2422-2423 213. 2424-2425 214. 2426-2427 215. 2428-2429 216. 2430-2431 217. 2432-2433 218. 2434-2435 219. 2436-2437 220. 2438-2439 221.	
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FIGURE 8

CTCTGGAAGGTCACGGCCACAGGATTCCAACAGTGCTCCCTCATAGATGGACGAAAGTGTGA
CCCCCCTTTTCAGGCTTTTCAGGGGGACTGGTCCTCCTGGAGGAGATGCTCGCCTTGGGGAATA
ATCACTTTATTGGTTTTTGTGAATGATTCTGTGACTAAGTCTATTGTGGCTTTGCGCTTAACT
CTGGTGGTGAAGGTCAGCACCTGTGTGCCGGGGGAGAGTCACGCAAATGACTTGGAGTGTTC
AGGAAAAGGAAAATGCACCACGAAGCCGTCAGAGGCAACTTTTTTCCTGTACCTGTGAGGAGC
AGTACGTGGGTACTTTCTGTGAAGAATACGATGCTTGCCAGAGGAAACCTTGCCAAAACAAC
GCGAGCTGTATTGATGCAAATGAAAAGCAAGATGGGAGCAATTTACCTGTGTTTGCCTTCC
TGGTTATACTGGAGAGCTTTGCCAACCGAACTGAGATTGGAGCGAACGACCTACACCGAACT
GAGATAGGGGAG

[illegible]

FIGURE 9

GCTGAGTCTGCTGCTCCTGCTGCTGCTGCTCCAGCCTGTAACCTGTGCCTACACCACGCCAG
GCCCCCCCAGAGCCCTCACCACGCTGGGCGCCCCCAGAGCCCACACCATGCCGGGCACCTAC
GCTCCCTCGACCACACTCAGTAGTCCCAGCACCCAGGGCCTGCAAGAGCAGGCACGGGCCCT
GATGCGGGACTTCCCGCTCGTGGACGGCCACAACGACCTGCCCCCTGGTCCTAAGGCAGGTTT
ACCAGAAAGGGCTACAGGATGTTAACCTGCGCAATTTTCAGCTACGGCCAGACCAGCCTGGAC
AGGCTTAGAGATGGCCTCGTGGGCGCCCAGTTCTGGTCAGCCTATGTGCCATGCCAGACCCA
GGACCGGGATGCCCTGCGCCTCACCTGGAGCAGATTGACCTCATA CGCCGCATGTGTGCCT
CCTATTCTGAGCTGGAGCTTGTGACCTCGGCTAAAGCTCTGAACGACACTCAGAAATTGGCC
TGCCTCATCGGTGTAGAGGGTGGCCACTCGCTGGACAATAGCCTCTCCATCTTACGTACCTT
CTACATGCTGGGAGTGCGCTACCTGACGCTCACCCACACCTGCAACACACCCTGGGCAGAGA
GCTCCGCTAAGGGCGTCCACTCCTTCTACAACAACATCAGCGGGCTGACTGACTTTGGTGAG
AAGGTGGTGGCAGAAATGAACCGCCTGGGCATGATGGTAGACTTATCCCATGTCTCAGATGC
TGTGGCACGGCGGGCCCTGGAAGTGTACAGGCACCTGTGATCTTCTCCCACTCGGCTGCCC
GGGTGTGTGCAACAGTGCTCGGAATGTTCTGATGACATCCTGCAGCTTCTGAAGAAGAAC
GGTGGCGTCGTGATGGTGTCTTTGTCCATGGGAGTAATACAGTGCAACCCATCAGCCAATGT
GTCCACTGTGGCAGATCACTTCGACCACATCAAGGCTGTCATTGGATCCAAGTTCATCGGGA
TTGGTGGAGATTATGATGGGGCCGGCAAATTCCCTCAGGGGCTGGAAGACGTGTCCACATAC
CCGGTCCTGATAGAGGAGTTGCTGAGTCGTGGCTGGAGTGAGGAAGAGCTTCAGGGTGTCTT
TCGTGGAAACCTGCTGCGGGTCTTCAGACAAGTGGAAAAGGTACAGGAAGAAAACAAATGGC
AAAGCCCCCTTGAGGACAAGTTCCCGGATGAGCAGCTGAGCAGTTCCTGCCACTCCGACCTC
TCACGTCTGCGTCAGAGACAGAGTCTGACTTCAGGCCAGGAACTCACTGAGATTCCCATACA
CTGGACAGCCAAGTTACCAGCCAAGTGGTCAGTCTCAGAGTCCTCCCCCCACATGGCCCCAG
TCCTTGCAGTTGTGGCCACCTTCCCAGTCCTTATTCTGTGGCTCTGATGACCCAGTTAGTCC
TGCCAGATGTCACTGTAGCAAGCCACAGACACCCACAAAGTTCCTGTTGTGCAGGCACA
AATATTTCTGAAATAAATGTTTTGGACATAG

[illegible]

<MW: 47787, pI: 6.11, NX(S/T): 5

N-glycosylation sites.

N-myristoylation sites.

Renal dipeptidase active site.

amino acids 134-157

FIGURE 11

AAAACCTATAAATATTCCGGATTATTCATACCGTCCCACCATCGGGCGCGGATCCGCGGCCG
CGAATTCTAAACCAACATGCCGGGCACCTACGCTCCCTCGACCACACTCAGTAGTCCCAGCA
CCCAGGGCCTGCAAGAGCAGGCACGGGCCCTGATGCGGGACTTCCCGCTCGTGGACGGCCAC
AACGACCTGCCCCCTGGTCCTAAGGCAGGTTTACCAGAAAGGGCTACAGGATGTTAACCTGCG
CAATTTTCAGCTACGGCCAGACCAGCCTGGACAGGCTTAGAGATGGCCTCGTGGGCGCCCAGT
TCTGGTCAGCCTATGTGCCATGCCAGACCCAGGACCGGGATGCCCTGCGCCTCACCTGGAG
CAGATTGACCTCATACGCCGCATGTGTGCCTCCTATTCTGAGCTGGAGCTTGTGACCTCGGC
TAAAGCTCTGAACGACACTCAGAAATTGGCCTGCCTCATCGGTGTAGAGGGTGGCCACTCGC
TGGACAATAGCCTCTCCATCTTACGTACCTTCTACATGCTGGGAGTGCGCTACCTGACGCTC
ACCCACACCTGCAACACACCCTGGGCAGAGAGCTCCGCTAAGGGCGTCCACTCCTTCTACAA
CAACATCAGCGGGCTGACTGACTTTGGTGAGAAGGTGGTGGCAGAAATGAACCGCCTGGGCA
TGATGGTAGACTTATCCCATGTCTCAGATGCTGTGGCACGGCGGGCCCTGGAAGTGTCACAG
GCACCTGTGATCTTCTCCCCTCGGCTGCCCCGGGGTGTGTGCAACAGTGCTCGGAATGTTCC
TGATGACATCCTGCAGCTTCTGAAGAAGAACGGTGGCGTCGTGATGGTGTCTTTGTCCATGG
GAGTAATACAGTGCAACCCATCAGCCAATGTGTCCACTGTGGCAGATCACTTCGACCACATC
AAGGCTGTCATTGGATCCAAGTTCATCGGGATTGGTGGAGATTATGATGGGGCCGGCAAATT
CCCTCAGGGGCTGGAAGACGTGTCCACATACCCGGTCCTGATAGAGGAGTTGCTGAGTCGTG
GCTGGAGTGAGGAAGAGCTTCAGGGTGTCTTCGTGGAAACCTGCTGCGGGTCTTCAGACAA
GTGGAAAAGGTACAGGAAGAAAACAAATGGCAAAGCCCCTTGGAGGACAAGTTCCCGGATGA
GCAGCTGAGCAGTTCCTGCCACTCCGACCTCTCACGTCTGCGTCAGAGACAGAGTCTGACTT
CAGGCCAGGAACTCACTGAGATTCCCATACTGGACAGCCAAGTTACCAGCCAAGTGGTCA
GTCTCAGAGTCCTCCCCCACCCTGACAAAACCTCACACATGCCCACCGTGCCCAGCACCTGA
ACTCCTGGGGGGACCGTCAGTCTTCTTCCCCC AAAACCCAAGGACACC

FIGURE 12

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA35872

><subunit 1 of 1, 446 aa, 0 stop

><NX(S/T): 5

MPGTYAPSTTLSSPSTQGLQEQARALMRDFPLVDGHNDLPLVLRQVYQKGLQDVNLRNFSYG
QTSLDRLRDGLVGAQFWSAYVPCQTQDRDALRLTLEQIDLIRMCASYSELELVTSAKALND
TQKLACLIGVEGGHSLDNSLSILRTFYMLGVRYLTLTHTCNTPWAESSAKGVHSFYNNISGL
TDFGEKVVAEMNRLGMMVDLSHVSDAVARRALEVSQAPVIFSHSAARGVCNSARNVPDDILQ
LLKKNNGGVVMVSLSMGVIQCNPSANVSTVADHFDHIKAVIGSKFIGIGGDYDGAGKFPQGLE
DVSTYPVLIEELLSRGWSEEELQGVLRGNLLRVFRQVEKVQEENKWQSPLEDKFPDEQLSSS
CHSDLSRLRQRQSLTSGQELTEIPIHWTAKLPAKWSVSESSPHPKTHTCPPCPAPELLGGP
SVFLFPPKPKDT

09443 0330 224650

Section 1		Section 2		Section 3		Section 4		Section 5		Section 6		Section 7		Section 8		Section 9		Section 10		Section 11		Section 12		Section 13		Section 14		Section 15		Section 16		Section 17		Section 18		Section 19		Section 20		Section 21		Section 22		Section 23		Section 24		Section 25		Section 26		Section 27		Section 28		Section 29		Section 30		Section 31		Section 32		Section 33		Section 34		Section 35		Section 36		Section 37		Section 38		Section 39		Section 40		Section 41		Section 42		Section 43		Section 44		Section 45		Section 46		Section 47		Section 48		Section 49		Section 50		Section 51		Section 52		Section 53		Section 54		Section 55		Section 56		Section 57		Section 58		Section 59		Section 60		Section 61		Section 62		Section 63		Section 64		Section 65		Section 66		Section 67		Section 68		Section 69		Section 70		Section 71		Section 72		Section 73		Section 74		Section 75		Section 76		Section 77		Section 78		Section 79		Section 80		Section 81		Section 82		Section 83		Section 84		Section 85		Section 86		Section 87		Section 88		Section 89		Section 90		Section 91		Section 92		Section 93		Section 94		Section 95		Section 96		Section 97		Section 98		Section 99		Section 100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																																																																																																				

Section 1		Section 2		Section 3		Section 4		Section 5		Section 6		Section 7		Section 8		Section 9		Section 10		Section 11		Section 12		Section 13		Section 14		Section 15		Section 16		Section 17		Section 18		Section 19		Section 20		Section 21		Section 22		Section 23		Section 24		Section 25		Section 26		Section 27		Section 28		Section 29		Section 30		Section 31		Section 32		Section 33		Section 34		Section 35		Section 36		Section 37		Section 38		Section 39		Section 40		Section 41		Section 42		Section 43		Section 44		Section 45		Section 46		Section 47		Section 48		Section 49		Section 50		Section 51		Section 52		Section 53		Section 54		Section 55		Section 56		Section 57		Section 58		Section 59		Section 60		Section 61		Section 62		Section 63		Section 64		Section 65		Section 66		Section 67		Section 68		Section 69		Section 70		Section 71		Section 72		Section 73		Section 74		Section 75		Section 76		Section 77		Section 78		Section 79		Section 80		Section 81		Section 82		Section 83		Section 84		Section 85		Section 86		Section 87		Section 88		Section 89		Section 90		Section 91		Section 92		Section 93		Section 94		Section 95		Section 96		Section 97		Section 98		Section 99		Section 100	
1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100																																																																																																				

FIGURE 14

><ss.DNA38113

><subunit 1 of 1, 422 aa, 1 stop

><MW: 46302, pI: 9.42, NX(S/T): 6

MPAGRRGPAAQSARRPPPLLPLLLLLLCVLGAPRAGSGAHTAVISPODPTLLIGSSLLATCSV
HGDPPGATAEGLYWTLNGRRLPPELSRVLNASTLALALANLNGSRQRSGDNLVCHARDGSIL
AGSCLYVGLPPEKPVNISCWSKNMKDLTCRWTPGAHGETFLHTNYSKYKLRWYGQDNTCEE
YHTVGPHSCHIPKDLALFTPYEIWVEATNRLGSARSDVLTLDILDVVTTPPPDVHVS RVGG
LEDQLSVRWVSPALKDFLFQAKYQIRYRVEDSVDWKVVDDVSNQTSCRLAGLKPGTVYFVQ
VRCNPFGIYGSKKAGIWSEWSHPTAASTPRSERPGPGGGACEPRGGEPSSGPVRRELKQFLG
WLKKHAYCSNLSFRLYDQWRAWMQKSHKTRNQDEGILPSGRRGTARGPAR

Signal sequence.

amino acids 1-30

Transmembrane domain.

amino acids 44-61

N-glycosylation sites.

amino acids 92-96, 104-108, 140-144, 168-172, 292-296, 382-386

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 413-417

N-myristoylation sites.

amino acids 30-36, 37-43, 73-79, 121-127, 179-185, 218-224,
300-306, 317-323, 320-326, 347-353, 355-361, 407-413

Amidation site.

amino acids 3-7, 79-83, 411-415

Growth factor and cytokines receptors family signature 2.

amino acids 325-331

TOOEBO"2E4460

	1990-1991	1991-1992	1992-1993	1993-1994	1994-1995	1995-1996	1996-1997	1997-1998	1998-1999	1999-2000	2000-2001	2001-2002	2002-2003	2003-2004	2004-2005	2005-2006	2006-2007	2007-2008	2008-2009	2009-2010	2010-2011	2011-2012	2012-2013	2013-2014	2014-2015	2015-2016	2016-2017	2017-2018	2018-2019	2019-2020	2020-2021	2021-2022	2022-2023	2023-2024	2024-2025	2025-2026	2026-2027	2027-2028	2028-2029	2029-2030	2030-2031	2031-2032	2032-2033	2033-2034	2034-2035	2035-2036	2036-2037	2037-2038	2038-2039	2039-2040	2040-2041	2041-2042	2042-2043	2043-2044	2044-2045	2045-2046	2046-2047	2047-2048	2048-2049	2049-2050	2050-2051	2051-2052	2052-2053	2053-2054	2054-2055	2055-2056	2056-2057	2057-2058	2058-2059	2059-2060	2060-2061	2061-2062	2062-2063	2063-2064	2064-2065	2065-2066	2066-2067	2067-2068	2068-2069	2069-2070	2070-2071	2071-2072	2072-2073	2073-2074	2074-2075	2075-2076	2076-2077	2077-2078	2078-2079	2079-2080	2080-2081	2081-2082	2082-2083	2083-2084	2084-2085	2085-2086	2086-2087	2087-2088	2088-2089	2089-2090	2090-2091	2091-2092	2092-2093	2093-2094	2094-2095	2095-2096	2096-2097	2097-2098	2098-2099	2099-2100	2100-2101	2101-2102	2102-2103	2103-2104	2104-2105	2105-2106	2106-2107	2107-2108	2108-2109	2109-2110	2110-2111	2111-2112	2112-2113	2113-2114	2114-2115	2115-2116	2116-2117	2117-2118	2118-2119	2119-2120	2120-2121	2121-2122	2122-2123	2123-2124	2124-2125	2125-2126	2126-2127	2127-2128	2128-2129	2129-2130	2130-2131	2131-2132	2132-2133	2133-2134	2134-2135	2135-2136	2136-2137	2137-2138	2138-2139	2139-2140	2140-2141	2141-2142	2142-2143	2143-2144	2144-2145	2145-2146	2146-2147	2147-2148	2148-2149	2149-2150	2150-2151	2151-2152	2152-2153	2153-2154	2154-2155	2155-2156	2156-2157	2157-2158	2158-2159	2159-2160	2160-2161	2161-2162	2162-2163	2163-2164	2164-2165	2165-2166	2166-2167	2167-2168	2168-2169	2169-2170	2170-2171	2171-2172	2172-2173	2173-2174	2174-2175	2175-2176	2176-2177	2177-2178	2178-2179	2179-2180	2180-2181	2181-2182	2182-2183	2183-2184	2184-2185	2185-2186	2186-2187	2187-2188	2188-2189	2189-2190	2190-2191	2191-2192	2192-2193	2193-2194	2194-2195	2195-2196	2196-2197	2197-2198	2198-2199	2199-2200	2200-2201	2201-2202	2202-2203	2203-2204	2204-2205	2205-2206	2206-2207	2207-2208	2208-2209	2209-2210	2210-2211	2211-2212	2212-2213	2213-2214	2214-2215	2215-2216	2216-2217	2217-2218	2218-2219	2219-2220	2220-2221	2221-2222	2222-2223	2223-2224	2224-2225	2225-2226	2226-2227	2227-2228	2228-2229	2229-2230	2230-2231	2231-2232	2232-2233	2233-2234	2234-2235	2235-2236	2236-2237	2237-2238	2238-2239	2239-2240	2240-2241	2241-2242	2242-2243	2243-2244	2244-2245	2245-2246	2246-2247	2247-2248	2248-2249	2249-2250	2250-2251	2251-2252	2252-2253	2253-2254	2254-2255	2255-2256	2256-2257	2257-2258	2258-2259	2259-2260	2260-2261	2261-2262	2262-2263	2263-2264	2264-2265	2265-2266	2266-2267	2267-2268	2268-2269	2269-2270	2270-2271	2271-2272	2272-2273	2273-2274	2274-2275	2275-2276	2276-2277	2277-2278	2278-2279	2279-2280	2280-2281	2281
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[illegible]

FIGURE 16

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436

<subunit 1 of 1, 300 aa, 1 stop

<MW: 32964, pI: 9.52, NX(S/T): 1

MKFLLDILLLLPLLVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACKCKGLGAKVHTFVVDCSNREDIYSSAKKVKAIEIGDVSILVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHVSVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTSLGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence.

amino acids 1-19

Transmembrane domain.

amino acids 170-187

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 30-34, 283-287

N-myristoylation sites.

amino acids 43-49, 72-78, 122-128, 210-216

054436-03001
"seqdb2/sst/DNA/Dnaseqs.full/ss.DNA34436"

FIGURE 17

GACTAGTTCTCTTGGAGTCTGGGAGGAGGAAAGCGGAGCCGGCAGGGAGCGAACCAGGACTG
GGGTGACGGCAGGGCAGGGGGCGCCTGGCCGGGGGAGAAGCGCGGGGGGCTGGAGCACCACCAA
CTGGAGGGTCCGGAGTAGCGAGCGCCCCGAAGGAGGCCATCGGGGAGCCGGGAGGGGGGACT
GCGAGAGGACCCCGGCGTCCGGGGCTCCCGGTGCCAGCGCTATGAGGCCACTCCTCGTCCTGC
TGCTCCTGGGCCTGGCGGGCCGGCTCGCCCCCACTGGACGACAACAAGATCCCCAGCCTCTGC
CCGGGGCACCCTTCCAGGCACGCCGGGGCCACCATGGCAGCCAGGGCTTGCCGGGGCCG
CGATGGCCGCGACGGCCGCGACGGCGCGCCCCGGGGCTCCGGGAGAGAAAGGCGAGGGCGGGGA
GGCCGGGACTGCCGGGACCTCGAGGGGACCCCGGGCCGCGAGGAGAGGCGGGACCCGCGGGG
CCCACCGGGCCTGCCGGGGAGTGCTCGGTGCCTCCGCGATCCGCCTTCAGCGCCAAGCGCTC
CGAGAGCCGGGTGCCTCCGCCGTCTGACGCACCCTTGCCCTTCGACCGCGTGCTGGTGAACG
AGCAGGGACATTACGACGCCGTCAACGGCAAGTTCACCTGCCAGGTGCCTGGGGTCTACTAC
TTCGCCGTCCATGCCACCGTCTACCGGGCCAGCCTGCAGTTTGATCTGGTGAAGAATGGCGA
ATCCATTGCCTCTTTCTTCCAGTTTTTCGGGGGGTGGCCCAAGCCAGCCTCGCTCTCGGGGG
GGCCCATGGTGAGGCTGGAGCCTGAGGACCAAGTGTGGGTGCAGGTGGGTGTGGGTGACTAC
ATTGGCATCTATGCCAGCATCAAGACAGACAGCACCTTCTCCGGATTTCTGGTGTACTCCGA
CTGGCACAGCTCCCCAGTCTTTGCTTAGTGCCCACTGCAAAGTGAGCTCATGCTCTCACTCC
TAGAAGGAGGGTGTGAGGCTGACAACCAGGTCATCCAGGAGGGCTGGCCCCCCTGGAATATT
GTGAATGACTAGGGAGGTGGGGTAGAGCACTCTCCGTCCTGCTGCTGGCAAGGAATGGGAAC
AGTGGCTGTCTGCGATCAGGTCTGGCAGCATGGGGCAGTGGCTGGATTTCTGCCCCAAGACCA
GAGGAGTGTGCTGTGCTGGCAAGTGTAAGTCCCCCAGTTGCTCTGGTCCAGGAGCCCACGGT
GGGGTGCTCTCTTCCTGGTCCTCTGCTTCTCTGGATCCTCCCCACCCCCTCCTGCTCCTGGG
GCCGGCCCTTTTCTCAGAGATCACTCAATAAACCTAAGAACCCTCATAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

FIGURE 18

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA40592

><subunit 1 of 1, 243 aa, 1 stop

><MW: 25298, pI: 6.44, NX(S/T): 0

MRPLLVLALLGLAAGSPPLDDNKIPSLCPGHPGLPGTPGHHGSQGLPGRDGRDGRDGAPGAP
GEKGEGRPGLPGPRGDPGPRGEAGPAGPTGPAGECSVPPRSAFSAKRSESRVPPPSDAPLP
FDRVLVNEQGHYDAVTGKFTCQVPGVYYFAVHATVYRASLQFDLVKNGESIASFFQFFGGWP
KPASLSGGAMVRLEPEDQVWVQVGVDYIGIYASIKTDSTFSGFLVYSDWHSSPVFA

Signal sequence.

amino acids 1-15

N-myristoylation sites.

amino acids 11-17, 68-74, 216-222

Cell attachment sequence.

amino acids 77-80

09443-24460

FIGURE 19

CTCTTTTGTCCACCAGCCCAGCCTGACTCCTGGAGATTGTGAATAGCTCCATCCAGCCTGAG
AAACAAGCCGGGTGGCTGAGCCAGGCTGTGCACGGAGCACCTGACGGGCCCCAACAGACCCAT
GCTGCATCCAGAGACCTCCCCTGGCCGGGGGCATCTCCTGGCTGTGCTCCTGGCCCTCCTTG
GCACCACCTGGGCAGAGGTGTGGCCACCCCAGCTGCAGGAGCAGGCTCCGATGGCCGGAGCC
CTGAACAGGAAGGAGAGTTCCTTGCTCCTCTCCCTGCACAACCGCCTGCGCAGCTGGGTCCA
GCCCCCTGCGGCTGACATGCGGAGGCTGGACTGGAGTGACAGCCTGGCCCAACTGGCTCAAG
CCAGGGCAGCCCTCTGTGGAATCCCAACCCCGAGCCTGGCATCCGGCCTGTGGCGCACCCCTG
CAAGTGGGCTGGAACATGCAGCTGCTGCCCCGCGGGCTTGGCGTCCTTTGTTGAAGTGGTCAG
CCTATGGTTTGCAGAGGGGCAGCGGTACAGCCACGCGGCAGGAGAGTGTGCTCGCAACGCCA
CCTGCACCCACTACACGCAGCTCGTGTGGGCCACCTCAAGCCAGCTGGGCTGTGGGCGGCAC
CTGTGCTCTGCAGGCCAGACAGCGATAGAAGCCTTTGTCTGTGCCTACTCCCCCGGAGGCAA
CTGGGAGGTCAACGGGAAGACAATCATCCCCTATAAGAAGGGTGCCTGGTGTTCGCTCTGCA
CAGCCAGTGTCTCAGGCTGCTTCAAAGCCTGGGACCATGCAGGGGGGCTCTGTGAGGTCCCC
AGGAATCCTTGTGCGCATGAGCTGCCAGAACCATGGACGTCTCAACATCAGCACCTGCCACTG
CCACTGTCCCCCTGGCTACACGGGCAGATACTGCCAAGTGAGGTGCAGCCTGCAGTGTGTGC
ACGGCCGGTTCCGGGAGGAGGAGTGCTCGTGCGTCTGTGACATCGGCTACGGGGGAGCCCAG
TGTGCCACCAAGGTGCATTTTCCCTTCCACACCTGTGACCTGAGGATCGACGGAGACTGCTT
CATGGTGTCTTCAGAGGCAGACACCTATTACAGAGCCAGGATGAAATGTCAGAGGAAAGGCG
GGGTGCTGGCCCAGATCAAGAGCCAGAAAGTGACAGGACATCCTCGCCTTCTATCTGGGCCGC
CTGGAGACCACCAACGAGGTGACTGACAGTGACTTCGAGACCAGGAACTTCTGGATCGGGCT
CACCTACAAGACCGCCAAGGACTCCTTCCGCTGGGCCACAGGGGAGCACCAAGGCCTTCACCA
GTTTTGCCTTTGGGCAGCCTGACAACCACGGGCTGGTGTGGCTGAGTGCTGCCATGGGGTTT
GGCAACTGCGTGGAGCTGCAGGCTTCAGCTGCCTTCAACTGGAACGACCAGCGCTGCAAAAC
CCGAAACCGTTACATCTGCCAGTTTGCCCAGGAGCACATCTCCCGGTGGGGCCCAGGGTCCTI
GAGGCCTGACCACATGGCTCCCTCGCCTGCCCTGGGAGCACCGGCTCTGCTTACCTGTCTGC
CCACCTGTCTGGAACAAGGGCCAGGTAAAGACCACATGCCTCATGTCCAAGAGGTCTCAGA
CCTTGCACAATGCCAGAAGTTGGGCAGAGAGAGGCAGGGAGGCCAGTGAGGGCCAGGGAGTG
AGTGTTAGAAGAAGCTGGGGCCCTTCGCCTGCTTTTGATTGGGAAGATGGGCTTCAATTAGA
TGGCGAAGGAGAGGACACCGCCAGTGGTCCAAAAAGGCTGCTCTCTTCCACCTGGCCCAGAC
CCTGTGGGGCAGCGGAGCTTCCCTGTGGCATGAACCCACGGGGTATTAAATTATGAATCAG
CTGAAAAAAAAAAAAA

FIGURE 20

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44176

<subunit 1 of 1, 455 aa, 1 stop

<MW: 50478, pI: 8.44, NX(S/T): 2

MLHPETSPGRGHLLAVLLALLGTTWAEVWPPQLQEQAPMAGALNRKESFLLLSLHNRLRSWV
QPPAADMRRLDWSDSLAQLAQARAALCGIPTPSLASGLWRTLQVGWNMQLLPAGLASFVEVV
SLWFAEGQRYSHAAGECARNATCTHYTQLVWATSSQLGCGRHLCSAGQTAIEAFVCAYSPPG
NWEVNGKTIIPYKKGAWCSLCTASVSGCFKAWDHAGGLCEVPRNPCRMSCQNHGRLNISTCH
CHCPPGYTGRYCQVRCSLQCVHGRFREEECSCVCDIGYGGAQCATKVHFPFHTCDLRIDGDC
FMVSSEADTYRARMKCQRKGGVLAQIKSQKVQDILAFYLGRLETTNEVTDSDFETRNF
WIG
LTYKTAKDSFRWATGEHQAFTSFAFGQPDNHGLVWLSAAMGFGNCVELQASAAFNWNDQRCK
TRNRYICQFAQEHISRWGPGS

Signal sequence.

amino acids 1-26

Transmembrane domain.

amino acids 110-124

N-glycosylation sites.

amino acids 144-148, 243-247

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 45-49

N-myristoylation sites.

amino acids 22-28, 99-105, 131-137, 201-207, 213-219, 287-293,
288-294, 331-337, 398-404

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 204-215

EGF-like domain cysteine pattern signature.

amino acids 249-261, 280-292

C-type lectin domain signature.

amino acids 417-442

05944432E4460F00E802E4460

Descriptive statistics		Descriptive statistics		Descriptive statistics		Descriptive statistics		Descriptive statistics			
Variable	Mean	SD	Variable	Mean	SD	Variable	Mean	SD	Variable	Mean	SD
Age	35.2	12.5	Gender	Male	65.2	Female	34.8	12.1	Marital status	Married	68.5
Education	12.5	2.1	Occupation	Manager	25.5	Worker	74.5	3.2	Religion	Christian	85.2
Income	15.2	4.5	Health status	Good	78.5	Fair	21.5	1.8	Political party	Democrat	62.5
Family size	3.2	1.5	Home ownership	Owned	72.5	Rented	27.5	2.5	Volunteer work	Yes	55.2
Life satisfaction	7.5	1.2	Life satisfaction	7.5	1.2	Life satisfaction	7.5	1.2	Life satisfaction	7.5	1.2

AA



FIGURE 23

CGGACGCGTGGGGTGCCCCGACATGGCGAGTGTAGTGCTGCCGAGCGGATCCCAGTGTGCGGC
GGCAGCGGCGGCGGCGGCGCCTCCCGGGCTCCGGCTTCTGCTGTTGCTCTTCTCCGCCGCGG
CACTGATCCCCACAGGTGATGGGCAGAAATCTGTTTACGAAAGACGTGACAGTGATCGAGGGA
GAGGTTGCGACCATCAGTTGCCAAGTCAATAAGAGTGACGACTCTGTGATTCAGCTACTGAA
TCCCAACAGGCAGACCATTTATTTTCAGGGACTTCAGGCCTTTGAAGGACAGCAGGTTTCAGT
TGCTGAATTTTTCTAGCAGTGAACCTCAAAGTATCATTGACAAACGTCTCAATTTCTGATGAA
GGAAGATACTTTTGCCAGCTCTATACCGATCCCCCACAGGAAAGTTACACCACCATCACAGT
CCTGGTCCCACCACGTAATCTGATGATCGATATCCAGAAAGACACTGCGGTGGAAGGTGAGG
AGATTGAAGTCAACTGCACTGCTATGGCCAGCAAGCCAGCCACGACTATCAGGTGGTTCAAA
GGGAACACAGAGCTAAAAGGCAAATCGGAGGTGGAAGAGTGGTCAGACATGTACACTGTGAC
CAGTCAGCTGATGCTGAAGGTGCACAAGGAGGACGATGGGGTCCCAGTGATCTGCCAGGTGG
AGCACCTTGCGGTCACTGGAAACCTGCAGACCCAGCGGTATCTAGAAGTACAGTATAAGCCT
CAAGTGCACATTCAGATGACTTATCCTCTACAAGGCTTAACCCGGGAAGGGGACGCGCTTGA
GTTAACATGTGAAGCCATCGGGAAGCCCCAGCCTGTGATGGTAACTTGGGTGAGAGTCGATG
ATGAAATGCCTCAACACGCCGTACTGTCTGGGCCCAACCTGTTTCATCAATAACCTAAACAAA
ACAGATAATGGTACATACCGCTGTGAAGCTTCAAACATAGTGGGGAAAGCTCACTCGGATTA
TATGCTGTATGTATACGATCCCCCCCACAACCTATCCCTCCTCCCACAACAACCACCACCACCA
CCACCACCACCACCACCACCATCCTTACCATCATCACAGATTCCCGAGCAGGTGAAGAAGGC
TCGATCAGGGCAGTGGATCATGCCGTGATCGGTGGCGTCGTGGCGGTGGTGGTGTTCGCCAT
GCTGTGCTTGCTCATCATTCTGGGGCGCTATTTTGCCAGACATAAAGGTACATACTTCACTC
ATGAAGCCAAAGGAGCCGATGACGCAGCAGACGCAGACACAGCTATAATCAATGCAGAAGGA
GGACAGAACAACTCCGAAGAAAAGAAAGAGTACTTCATCTAGATCAGCCTTTTTTGTTTCAAT
GAGGTGTCCAACCTGGCCCTATTTAGATGATAAAGAGACAGTGATATTGG



FIGURE 25

GGGGCGGGTGGACGCGGACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCCCTCGGGCCCCGA
CCCGCCAGGAAAGACTGAGGCCGCGGCCTGCCCCGCCCCGGCTCCCTGCGCCGCGCGCCGCTC
CCGGGACAGAAGATGTGCTCCAGGGTCCCTCTGCTGCTGCCGCTGCTCCTGCTACTGGCCCT
GGGGCCTGGGGTGCAGGGCTGCCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCT
GCACTGCCCCGCCAGGGGACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTAC
GTCTTTGAGAACGGCATCACCATGCTCGACGCAAGCAGCTTTGCCGGCCTGCCGGGCCTGCA
GCTCCTGGACCTGTCACAGAACCAGATCGCCAGCCTGCGCCTGCCCCGCCTGCTGCTGCTGG
ACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCATCCTGGACACTGCCAACGTGGAG
GCGCTGCGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACGAGGGGGCTCTTCAGCCGCTTGCG
CAACCTCCACGACCTGGATGTGTCCGACAACCAGCTGGAGCGAGTGCCACCTGTGATCCGAG
GCCTCCGGGGCCTGACGCGCCTGCGGCTGGCCGGCAACACCCGCATTGCCCAGCTGCGGGCC
GAGGACCTGGCCGGCCTGGCTGCCCTGCAGGAGCTGGATGTGAGCAACCTAAGCCTGCAGGC
CCTGCCTGGCGACCTCTCGGGCCTCTTCCCCCGCCTGCGGCTGCTGGCAGCTGCCCGCAACC
CCTTCAACTGCGTGTCGCCCTGAGCTGGTTTGGCCCCCTGGGTGCGCGAGAGCCACGTCACA
CTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCCGCCCCAAGAACGCTGGCCGGCTGCTCCT
GGAGCTTGACTACGCCGACTTTGGCTGCCCAGCCACCACCACACAGCCACAGTGCCCAACA
CGAGGCCCCGTGGTGCGGGAGCCCCACAGCCTTGTCTTCTAGCTTGGCTCCTACCTGGCTTAGC
CCCACAGCGCCGGCCACTGAGGCCCCCAGCCCGCCCTCCACTGCCCCACCGACTGTAGGGCC
TGTCCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTCAATGGGGGCACATGCCACCTGG
GGACACGGCACCACTGGCGTGCTTGTGCCCCGAAGGCTTCACGGGCCTGTACTGTGAGAGC
CAGATGGGGCAGGGGACACGGCCCAGCCCTACACCAGTCACGCCGAGGCCACCACGGTCCCT
GACCCTGGGCATCGAGCCGGTGAGCCCCACCTCCCTGCGCGTGGGGCTGCAGCGCTACCTCC
AGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTATCGCAACCTATCGGGCCCTGAT
AAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTGAGTACACGGTCACCCAGCTGCG
GCCCAACGCCACTTACTCCGTCTGTGTCATGCCTTTGGGGCCCCGGGCGGGTGCCGGAGGGCG
AGGAGGCCTGCGGGGAGGGCCATACACCCCCAGCCGTCCACTCCAACCACGCCCCAGTCACC
CAGGCCCCGCGAGGGCAACCTGCCGCTCCTCATTGCGCCCCGCCCTGGCCGCGGTGCTCCTGGC
CGCGCTGGCTGCGGTGGGGGCAGCCTACTGTGTGCGGCGGGGGCGGGCCATGGCAGCAGCGG
CTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGGCCCCCTGGAACCTGGAGGGAGTGAAGGTC
CCCTTGAGGCCAGGCCCCGAAGGCAACAGAGGGCGGTGGAGAGGCCCTGCCCAGCGGGTCTGA
GTGTGAGGTGCCACTCATGGGCTTCCCAGGGCCTGGCCTCCAGTCACCCCTCCACGCAAAGC
CCTACATCTAAGCCAGAGAGAGACAGGGCAGCTGGGGCCGGGCTCTCAGCCAGTGAGATGGC
CAGCCCCCTCCTGCTGCCACACCACGTAAGTTCTCAGTCCCAACCTCGGGGATGTGTGCAGA
CAGGGCTGTGTGACCACAGCTGGGCCCTGTTCCCTCTGGACCTCGGTCTCCTCATCTGTGAG
ATGCTGTGGCCCAGCTGACGAGCCCTAACGTCCCCAGAACCGAGTGCCCTATGAGGACAGTGT
CCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCGGGGCCCTGCCATGTGCTGGTAAC
GCATGCCTGGGCCCTGCTGGGCTCTCCCACTCCAGGCGGACCCTGGGGGCCAGTGAAGGAAG
CTCCCGGAAAGAGCAGAGGGAGAGCGGGTAGGCGGCTGTGTGACTCTAGTCTTGGCCCCAGG
AAGCGAAGGAACAAAAGAACTGGAAAGGAAGATGCTTTAGGAACATGTTTTTGCTTTTTTAA
AATATATATATATTTATAAGAGATCCTTTCCCATTTATTCTGGGAAGATGTTTTTCAAACCTC
AGAGACAAGGACTTTGGTTTTTTGTAAGACAAACGATGATATGAAGGCCTTTTGTAAGAAAAA
ATAAAAAA

09443-0304

Variable	Mean	SD	Min	Max
Age	38.5	12.5	25	65
Gender	0.5	0.5	0	1
Marital status	0.5	0.5	0	1
Education	12.5	2.5	9	16
Income	3500	1500	1000	8000
Health status	0.5	0.5	0	1
Smoking status	0.3	0.5	0	1
Alcohol consumption	0.2	0.4	0	1
Exercise frequency	0.5	0.5	0	1
Stress level	4.5	1.5	1	7
Sleep quality	0.5	0.5	0	1
Work satisfaction	0.5	0.5	0	1
Life satisfaction	0.5	0.5	0	1
Depression score	10.5	5.5	0	30
Anxiety score	15.5	7.5	0	40
Overall well-being	0.5	0.5	0	1

<MW: 63030, pI: 7.24, NX(S/T): 3

MCSRVP LLLP LLLLLLALGPGVQGCPSGCQCSQPQTVFCTARQGT TVPRDVP PDTVGLYVFEN
GITMLDASSFAGLPGLQLLDLSQNQIASLR LPRLLLLDL SHNSLLALEPGILD TANVEALRI
AGLGLQQLDEGLFSRLRNLHDL DVSDNQLERVPPVIRGLRGLTRLRLAGNTRIAQLRPEDLA
GLAALQE LDVSNLSLQALPGDLSGLFPRLRLLAAARNPFNCVCPLSWFGPWVRESHVTLASP
EETRCHFP PKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALSSSLAPT WLSPTAP
ATEAPSP PSTAPPTVGPVPQPQDCPPSTCLNGGTCHLGRHHLACLCPEGFTGLYCESQMGQ
GTRPSPTPVTPRPPRSLTLGIEPV SPTSLRVGLQRYLQGSSVQLRSLRLTYRNLSGPDKRLV
TLRLPASLA EYTVTQLRPNATYSVCVMPLGPGRVPEGEEACGEAHTPPAVHSNHAPVTQARE
GNLPLLIAPALAAVLLAALAAVGAAYCVRRGRAMAAAAQDKGQVGP GAGPLELEGVKVPLEP
GPKATEGGGEALPSGSECEVPLMGFP GPGLQSP L HAKPYI

amino acids 1-23

amino acids 501-522

amino acids 198-202, 425-429, 453-457

amino acids 262-270

amino acids 23-29, 27-33, 112-118, 273-279, 519-525, 565-571

amino acids 14-25

amino acids 355-367

amino acids 122-144, 194-216

General Data		Geographical Data		Economic Data		Social Data		Environmental Data																														
Variable	Value	Variable	Value	Variable	Value	Variable	Value	Variable	Value																													
Population	12,345,678	Area	567,890 km²	GDP	\$123,456,789	Unemployment	5.6%	Urbanization	78.9%																													
Gender Ratio	1.05	Coastline	1,234 km	Inflation	2.3%	Healthcare	85.4%	Deforestation	1.2%																													
Life Expectancy	74.5 years	Climate	Tropical	Interest Rate	4.5%	Education	92.1%	Biodiversity	High																													
Birth Rate	18.2‰	Soil Type	Volcanic	Trade Balance	Surplus	Literacy Rate	98.7%	Water Pollution	Low																													
Death Rate	10.1‰	Vegetation	Forest	Foreign Debt	\$56,789M	Internet Use	67.8%	Air Quality	Good																													
Mortality Rate	1.2‰	Wildlife	Endemic	Export Value	\$23,456M	Mobile Phone	89.0%	Waste Management	Improving																													
Infant Mortality	0.8‰	Conservation	Protected	Import Value	\$34,567M	Government	Stable	Renewable Energy	15.6%																													
Maternal Mortality	0.5‰	Heritage	World	Balance of Payments	Surplus	Corruption	Low	Space Exploration	Active																													
Crude Birth Rate	15.4‰	Archaeology	Excavated	Current Account	Surplus	Transparency	High	Artificial Intelligence	Developing																													
Crude Death Rate	8.9‰	Historical Sites	Preserved	Capital Gains	Positive	Human Rights	Respected	Autonomous Vehicles	Testing																													
Crude Mortality Rate	1.1‰	Monuments	Restored	Dividend Yield	3.2%	Gender Equality	Improving	Drone Technology	Widespread																													
Infant Mortality Rate	0.7‰	Religious Sites	Active	Yield to Maturity	5.1%	Environmental Policy	Strict	Space Station	Planned																													
Maternal Mortality Rate	0.4‰	Historical Monuments	Well-maintained	Weighted Average	4.8%	Climate Change	Addressed	Space Shuttle	Retired																													
Crude Birth Rate	14.8‰	Archaeological Sites	Excavated	Sharpe Ratio	1.2	Renewable Energy	Invested	Space Program	Active																													
Crude Death Rate	8.5‰	Historical Sites	Preserved	Alpha <table border="1" <thead> <tr> <th>Asset</th> <th>Value</th> </tr> </thead> <tbody> <tr> <td>Stocks</td> <td>10.5%</td> </tr> <tr> <td>Bonds</td> <td>5.2%</td> </tr> <tr> <td>Real Estate</td> <td>8.1%</td> </tr> <tr> <td>Commodities</td> <td>3.4%</td> </tr> <tr> <td>Art</td> <td>12.3%</td> </tr> <tr> <td>Collectibles</td> <td>7.8%</td> </tr> <tr> <td>Private Equity</td> <td>9.6%</td> </tr> <tr> <td>Hedge Funds</td> <td>6.7%</td> </tr> <tr> <td>Private Debt</td> <td>4.5%</td> </tr> <tr> <td>Real Estate</td> <td>8.1%</td> </tr> <tr> <td>Commodities</td> <td>3.4%</td> </tr> <tr> <td>Art</td> <td>12.3%</td> </tr> <tr> <td>Collectibles</td> <td>7.8%</td> </tr> <tr> <td>Private Equity</td> <td>9.6%</td> </tr> <tr> <td>Hedge Funds</td> <td>6.7%</td> </tr> <tr> <td>Private Debt</td> <td>4.5%</td> </tr> </tbody>	Asset	Value	Stocks	10.5%	Bonds	5.2%	Real Estate	8.1%	Commodities	3.4%	Art	12.3%	Collectibles	7.8%	Private Equity	9.6%	Hedge Funds	6.7%	Private Debt	4.5%	Real Estate	8.1%	Commodities	3.4%	Art	12.3%	Collectibles	7.8%	Private Equity	9.6%	Hedge Funds	6.7%	Private Debt	4.5%
Asset	Value																																					
Stocks	10.5%																																					
Bonds	5.2%																																					
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Commodities	3.4%																																					
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Art	12.3%																																					
Collectibles	7.8%																																					
Private Equity	9.6%																																					
Hedge Funds	6.7%																																					
Private Debt	4.5%																																					

 Space Exploration | Active || Crude Mortality Rate | 1.0‰ | Monuments | Restored | Beta| Asset | Value | | --- | --- | | Stocks | 10.5% | | Bonds | 5.2% | | Real Estate | 8.1% | | Commodities | 3.4% | | Art | 12.3% | | Collectibles | 7.8% | | Private Equity | 9.6% | | Hedge Funds | 6.7% | | Private Debt | 4.5% | | Real Estate | 8.1% | | Commodities | 3.4% | | Art | 12.3% | | Collectibles | 7.8% | | Private Equity | 9.6% | | Hedge Funds | 6.7% | | Private Debt | 4.5% | | Space Exploration | Active |
Infant Mortality Rate	0.6‰	Historical Sites	Preserved	Gamma	Asset	Value		---	---		Stocks	10.5%		Bonds	5.2%		Real Estate	8.1%		Commodities	3.4%		Art	12.3%		Collectibles	7.8%		Private Equity	9.6%		Hedge Funds	6.7%		Private Debt	4.5%		Real Estate	8.1%		Commodities	3.4%		Art	12.3%		Collectibles	7.8%		Private Equity	9.6%		Hedge Funds	6.7%		Private Debt	4.5%		Space Exploration	Active
Maternal Mortality Rate	0.3‰	Archaeological Sites	Excavated	Delta	Asset	Value		---	---		Stocks	10.5%		Bonds	5.2%		Real Estate	8.1%		Commodities	3.4%		Art	12.3%		Collectibles	7.8%		Private Equity	9.6%		Hedge Funds	6.7%		Private Debt	4.5%		Real Estate	8.1%		Commodities	3.4%		Art	12.3%		Collectibles	7.8%		Private Equity	9.6%		Hedge Funds	6.7%		Private Debt	4.5%		Space Exploration	Active
Crude Birth Rate	14.2‰	Historical Monuments	Well-maintained	Epsilon	Asset	Value		---	---		Stocks	10.5%		Bonds	5.2%		Real Estate	8.1%		Commodities	3.4%		Art	12.3%		Collectibles	7.8%		Private Equity	9.6%		Hedge Funds	6.7%		Private Debt	4.5%		Real Estate	8.1%		Commodities	3.4%		Art	12.3%		Collectibles	7.8%		Private Equity	9.6%		Hedge Funds	6.7%		Private Debt	4.5%		Space Exploration	Active
Crude Death Rate	8.2‰	Monuments	Restored	Zeta	Asset	Value		---	---																																																			

[illegible]

<subunit 1 of 1, 250 aa, 1 stop

MPASSPFLAPKGPPGNMGGPVREPALSVALWLSWGAALGAVACAMALLTQQTELQSLRREV

ATSKDDSDVTEVMWQPALRRGRGLQAQGYGVRIQDAGVYLLYSQVLFQDVTFTMGQVVSREG

QGRQETLFR CIRSMPSHPDRAYNSCYSAGVFHLHQGDILSVIIIPRARA KLNLSPHGTFLGFVKL

amino acids 1-40

amino acids 124-128

amino acids 156-164

amino acids 36-42, 40-46, 179-185, 242-248

amino acids 34-45

FIGURE 29

CACTTTCTCCCTCTCTTCCTTTACTTTTCGAGAAACCGCGCTTCCGCTTCTGGTTCGCAGAGAC
CTCGGAGACCGCGCCGGGGAGACGGAGGTGCTGTGGGTGGGGGGGACCTGTGGCTGCTCGTA
CCGCCCCCACCCTCCTCTTCTGCACTGCCGTCCTCCGGAAGACCTTTTCCCCTGCTCTGTT
TCCTTCACCGAGTCTGTGCATCGCCCCGGACCTGGCCGGGAGGAGGCTTGGCCGGCGGGAGA
TGCTCTAGGGGCGGCGCGGGAGGAGCGGCCGGCGGGACGGAGGGCCCCGGCAGGAAGATGGGC
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CCTGAGTCGTGTGCCCCATGTCCAGGGGGGAACAGCAGGAGTGGGAGGGGACTGAGGAGCTGC
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CTTTTCGGTGGGCCCGGAAGAAGCCCATGCACAGCAACCACTACTACCAGACGGTGATCTTCG
ACACGGAGTTCGTGAACCTCTACGACCACTTCAACATGTTCAACGGCAAGTTCTACTGCTAC
GTGCCCCGGCCTCTACTTCTTCAGCCTCAACGTGCACACCTGGAACCAGAAGGAGACCTACCT
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TCATGCAAAGCCAGAGCCTGATGCTGGAGCTGCGAGAGCAGGACCAGGTGTGGGTACGCCTC
TACAAGGGCGAACGTGAGAACGCCATCTTCAGCGAGGAGCTGGACACCTACATCACCTTCAG
TGGCTACCTGGTCAAGCACGCCACCGAGCCCCTAGCTGGCCGGCCACCTCCTTTCTCTCGCC
ACCTTCCACCCCTGCGCTGTGCTGACCCCAACGCCTCTTCCCCGATCCCTGGACTCCGACTC
CCTGGCTTTGGCATTCAGTGAGACGCCCTGCACACACAGAAAGCCAAAGCGATCGGTGCTCC
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GGCCTGCAGATGTTTCTATGAGGGGCAGAGCTCCTTGGTACATCCATGTGTGGCTCTGCTCC
ACCCCTGTGCCACCCCAAGAGCCCTGGGGGGTGGTCTCCATGCCTGCCACCCTGGCATCGGCT
TTCTGTGCCGCTCCACACAAATCAGCCCCAGAAGGCCCGGGGCTTGGCTTCTGTTTTT
TATAAAACACCTCAAGCAGCACTGCAGTCTCCCATCTCCTCGTGGGCTAAGCATCACCGCTT
CCACGTGTGTTGTGTTGGTTGGCAGCAAGGCTGATCCAGACCCCTTCTGCCCCCACTGCCCT
CATCCAGGCCTCTGACCAGTAGCCTGAGAGGGGCTTTTTCTAGGCTTCAGAGCAGGGGAGAG
CTGGAAGGGGCTAGAAAGCTCCCGCTTGTCTGTTTCTCAGGCTCCTGTGAGCCTCAGTCCTG
AGACCAGAGTCAAGAGGAAGTACACGTCCCAATCACCCGTGTCAGGATTCACCTCTCAGGAGC
TGGGTGGCAGGAGAGGCAATAGCCCCTGTGGCAATTGCAGGACCAGCTGGAGCAGGGTTGCG
GTGTCTCCACGGTGCTCTCGCCCTGCCCATGGCCACCCCAAGACTCTGATCTCCAGGAACCC
ATAGCCCCTCTCCACCTCACCCCATGTTGATGCCAGGGTCACTCTTGCTACCCGCTGGGCC
CCCAAACCCCGCTGCCTCTCTTCCTTCCCCCATCCCCACCTGGTTTTGAATAATCCTGC
TTCCCTCTCTGGGCCTGGCTGCCGGGATCTGGGGTCCCTAAGTCCCTCTCTTTAAAGAACTT
CTGCGGGTCAGACTCTGAAGCCGAGTTGCTGTGGGCGTGCCCGGAAGCAGAGCGCCACACTC
GCTGCTTAAGCTCCCCCAGCTCTTTCCAGAAAACATTAAACTCAGAATTGTGTTTTCAA

Variable	Mean	Standard deviation	Minimum	Maximum
Age	34.5	10.2	21	55
Gender	0.5	0.5	0	1
Marital status	0.6	0.5	0	1
Education	12.5	1.5	9	16
Income	15.2	5.8	5	35
Health status	0.8	0.4	0	1
Employment status	0.7	0.5	0	1
Home ownership	0.6	0.5	0	1
Vehicle ownership	0.5	0.5	0	1
Life satisfaction	4.2	1.8	1	7
Health-related quality of life	5.1	2.1	1	8
Physical functioning	6.5	2.5	1	10
Role limitations due to physical problems	3.2	1.5	1	5
Bodily pain	4.8	2.2	1	7
General health	5.5	2.0	1	8
Energy/fatigue	6.2	2.3	1	10
Emotional functioning	5.8	2.1	1	9
Social functioning	6.0	2.2	1	10
Healthcare use	2.5	1.2	1	4
Cost of healthcare	1.8	0.8	1	3
Access to healthcare	3.5	1.5	1	5
Health insurance coverage	0.9	0.3	0	1
Healthcare satisfaction	4.5	1.8	1	7
Healthcare utilization	2.8	1.3	1	4
Healthcare costs	1.5	0.7	1	3
Healthcare access	3.2	1.4	1	5
Healthcare quality	4.0	1.6	1	6
Healthcare equity	3.8	1.5	1	5
Healthcare efficiency	3.6	1.4	1	5
Healthcare effectiveness	3.4	1.3	1	5
Healthcare safety	3.2	1.2	1	5
Healthcare patient-centeredness	3.0	1.1	1	5
Healthcare transparency	2.8	1.0	1	5
Healthcare accountability	2.6	0.9	1	5
Healthcare integrity	2.4	0.8	1	5
Healthcare professionalism	2.2	0.7	1	5
Healthcare ethics	2.0	0.6	1	5
Healthcare governance	1.8	0.5	1	5
Healthcare leadership	1.6	0.4	1	5
Healthcare innovation	1.4	0.3	1	5
Healthcare research	1.2	0.2	1	5
Healthcare education	1.0	0.1	1	5
Healthcare training	0.8	0.1	1	5
Healthcare development	0.6	0.1	1	5
Healthcare improvement	0.4	0.1	1	5
Healthcare change	0.2	0.1	1	5
Healthcare transformation	0.1	0.1	1	5
Healthcare evolution	0.0	0.1	1	5
Healthcare revolution	0.0	0.1	1	5
Healthcare progress	0.0	0.1	1	5
Healthcare success	0.0	0.1	1	5
Healthcare achievement	0.0	0.1	1	5
Healthcare accomplishment	0.0	0.1	1	5
Healthcare fulfillment	0.0	0.1	1	5
Healthcare realization	0.0	0.1	1	5
Healthcare attainment	0.0	0.1	1	5
Healthcare completion	0.0	0.1	1	5
Healthcare conclusion	0.0	0.1	1	5
Healthcare end	0.0	0.1	1	5
Healthcare result	0.0	0.1	1	5
Healthcare outcome	0.0	0.1	1	5
Healthcare effect	0.0	0.1	1	5
Healthcare impact	0.0	0.1	1	5
Healthcare influence	0.0	0.1	1	5
Healthcare power	0.0	0.1	1	5
Healthcare force	0.0	0.1	1	5
Healthcare strength	0.0	0.1	1	5
Healthcare energy	0.0	0.1	1	5
Healthcare vitality	0.0	0.1	1	5
Healthcare dynamism	0.0	0.1	1	5
Healthcare activity	0.0	0.1	1	5
Healthcare motion	0.0	0.1	1	5
Healthcare change	0.0	0.1	1	5
Healthcare transformation	0.0	0.1	1	5
Healthcare evolution	0.0	0.1	1	5
Healthcare revolution	0.0	0.1	1	5
Healthcare progress	0.0	0.1	1	5
Healthcare success	0.0	0.1	1	5
Healthcare achievement	0.0	0.1	1	5
Healthcare accomplishment	0.0	0.1	1	5
Healthcare fulfillment	0.0	0.1	1	5
Healthcare realization	0.0	0.1	1	5
Healthcare attainment	0.0	0.1	1	5
Healthcare completion	0.0	0.1	1	5

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><subunit 1 of 1, 281 aa, 1 stop
```

MGSRGQGLLLAYCLLLAFASGLVLSRVPHVQGEQQEWEGTEELPSPPDHAERAEQHEKYRP
SQDQGLPASRCLRCCDPGTSMYPATAVPQINITILKGEKGDRGDRGLQGKYGKTGSAGARGH
TGPKGQKGSMPGERCKSHYAAFVGRKKPMHSNHYYQTVIFDTEFVNLYDHFNMTGKFY
CYVPGLYFFSLNVHTWNQKETYLHIMKNEEEVVILFAQVGDRSIMQSQSLMLELREQDQVWV
RLYKGERENAIIFSEELDTYITFSGYLVKHATEP

amino acids 1-25

amino acids 93-97

amino acids 7-13, 21-27, 67-73, 117-123, 129-135

amino acids 150-154

amino acids 104-107

[illegible]

GCGGAGCATCCGCTGCGGTCCTCGCCGAGACCCCGCGCGGATTCGCCGGTCCCTCCCGCGG
GCGCGACAGAGCTGTCCTCGCACCTGGATGGCAGCAGGGGCGCCGGGGTCCCTCTCGACGCCA
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CTTGACTTACACTTTGGTAATAATTTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
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GACAACCCAACTGCTACCTATTTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
CCAAGAGTTACCCCGAGGAAGATTCTCTCTTACATGGCCAATTTTCACAAGCAGTCACTCCCC
TAGCCCATCATCACACAGATTATTCAAAGCCCACCGATATCTCATGGAGAGACACACTTTCT
CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAATTTTCCTCTGATCAAGAAA
TAGCTCATCTGCTGCCTGAAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
CATACCACCTCGGCTACTCCAAAGCCCGCCACCCTTCTACCCACCAATGCTTCAGTGACACC
TTCTGGGACTTCCCAGCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
AGCCTCCCACGACCCTCATTTCTACAGTTTTTTACACGGGCTGCGGCTACACTCCAAGCAATG
GCTACAACAGCAGTTCTGACTACCACCTTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
AACCATAACGTTTACAGAAATCTCCAACCTTAACTTTGAACACAGGGAATGTGTATAACCCTA
CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCCTGGGAAGGT
AGGGAGGCCAGTCCAGGCAGTTCCTCCCAGGGCAGTGTTCCAGAAAATCAGTACGGCCTTCC
ATTTGAAAAATGGCTTCTTATCGGGTCCCTGCTCTTTGGTGTCTTGTTCCTGGTGATAGGCC
TCGTCCTCCTGGGTAGAATCCTTTCGGAATCACTCCGCAGGAAACGTTACTCAAGACTGGAT
TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAACCTCGGTGTCTCTTAATTCATT
TAGTAACCAGAAGCCCAAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTTG
TATTTTGAAGACAGGAAAATGCCCCCTTCTGCTTTTCTTTTTTTTTTTTGGAGACAGAGTCTT
GCTCTGTTGCCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGCAACCTCCGTCTC
CTGGGTTCAGCGATTCTCCTGCCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
CCACACCTGGGTGATTTTTTGTATTTTTTAGTAGAGACGGGGTTTTACCATGTTGGTCAGGCTG
GTCTCAAACCTCCTGACCTAGTGATCCACCCTCCTCGGCCTCCCAAAGTGCTGGGATTACAGG
CATGAGCCACCACAGCTGGCCCCCTTCTGTTTTATGTTTGGTTTTTTGAGAAGGAATGAAGTG
GGAACCAAATTAGGTAATTTTGGGTAATCTGTCTCTAAAATATTAGCTAAAAACAAAGCTCT
ATGTAAAGTAATAAAGTATAATTGCCATATAAATTTCAAATTCAACTGGCTTTTATGCAAA
GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTCTTGGTTCCAGATAAAATCAAC
TGTTTATATCAATTTCTAATGGATTTGCTTTTTCTTTTTATATGGATTCCTTTAAAACTTATT
CCAGATGTAGTTCCTTCCAATTAAATATTTGAATAAATCTTTTGTACTCAA

FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410

><subunit 1 of 1, 431 aa, 1 stop

><MW: 46810, pI: 6.45, NX(S/T): 6

MFFGGEGSLTYTLVIICFLTLRLSASQNCLKKSLEDVVIDIQSSLKSGIRGNEPVYTSTQED
CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
PTNASVTPSGTSQPQLATTAPPVTTVTSQPPTTLISTVFTRAAATLQAMATTAVLTTTFQAP
TDSKGSLETIPFTEISNLTGNTGNVYNPTALSMSNVESSTMNKTASWEGREASPGSSSQGSV
PENQYGLPFEEKWLLIGSLLFGVLFLVIGLVLLGRILSESLRRKRYSRDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 32

FIGURE 33

GCGGCACCTGGAAGATGCGCCCATTTGGCTGGTGGCCTGCTCAAGGTGGTGTTCGTGGTCTTC
GCCTCCTTGTGTGCCTGGTATTCGGGGTACCTGCTCGCAGAGCTCATTCCAGATGCACCCCT
GTCCAGTGCTGCCTATAGCATCCGCAGCATCGGGGAGAGGCCTGTCCTCAAAGCTCCAGTCC
CCAAAAGGCAAAAATGTGACCACTGGACTCCCTGCCCATCTGACACCTATGCCTACAGGTTA
CTCAGCGGAGGTGGCAGAAGCAAGTACGCCAAAATCTGCTTTGAGGATAACCTACTTATGGG
AGAACAGCTGGGAAATGTTGCCAGAGGAATAAACATTGCCATTGTCAACTATGTAACCTGGGA
ATGTGACAGCAACACGATGTTTTGATATGTATGAAGGCGATAACTCTGGACCGATGACAAAG
TTTATTCAGAGTGCTGCTCCAAAATCCCTGCTCTTCATGGTGACCTATGACGACGGAAGCAC
AAGACTGAATAACGATGCCAAGAATGCCATAGAAGCACTTGGAAGTAAAGAAATCAGGAACA
TGAAATTCAGGTCTAGCTGGGTATTTATTGCAGCAAAAGGCTTGGAACCTCCCTTCCGAAATT
CAGAGAGAAAAGATCAACCACTCTGATGCTAAGAACAACAGATATTCTGGCTGGCCTGCAGA
GATCCAGATAGAAGGCTGCATACCCAAAGAACGAAGCTTGACACTGCAGGGTCCTGAGTAAAT
GTGTTCTGTATAAACAAATGCAGCTGGAATCGCTCAAGAATCTTATTTTTCTAAATCCAACA
GCCCATATTTGATGAGTATTTTGGGTTTGTGTGTAACCAATGAACATTTGCTAGTTGTATCA
AATCTTGGTACGCAGTATTTTATACCAGTATTTTATGTAGTGAAGATGTCAATTAGCAGGA
AACTAAAATGAATGGAAATTCTTAAAAAAAAA

FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA46777

><subunit 1 of 1, 235 aa, 1 stop

><MW: 25982, pI: 9.09, NX(S/T): 2

MRPLAGGLLKVVVFVVFASLCAWYSGYLLAELIPDAPLSSAAYSIRSIGERPVLKAPVPKRQK
CDHWTPCPSDTYAYRLLSGGGRSKYAKICFEDNLLMGEQLGNVARGINIAIVNYVTGNVTAT
RCFDMYEGDNSGPMTKFIQSAAPKSLLFMVTYDDGSTRLNNDKNAIEALGSKEIRNMKFRS
SWVFIAAKGLELPSEIQREKINHSDAKNNRYSGWPAEIQIEGCIPKERS

Signal sequence.

amino acids 1-20

N-glycosylation sites.

amino acids 120-124, 208-212

Glycosaminoglycan attachment site.

amino acids 80-84

N-myristoylation sites.

amino acids 81-87, 108-114, 119-125

FOOEBD"2E4465D